

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Donnelly, John J
Dwarki, Varavani J
Liu, Margaret A
Montgomery, Donna L
Parker, Suzanne E
Shiver, John W

(ii) TITLE OF INVENTION: Nucleic Acid Pharmaceuticals - Influenza Matrix

(iii) NUMBER OF SEQUENCES: 64

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/461,268
(B) FILING DATE: 5-June-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/032,383
(B) FILING DATE: 18-May-1993

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 36,099
(C) REFERENCE/DOCKET NUMBER: 18972PIE

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGTGCACCT CAAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCTTTGAGA ATGTTGCACA TTC

23

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTACAAGAT CTACCATGCT TCTAACCGAG GTC

33

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC

36

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTATATAAGC AGAGCTCGTT TAG

23

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTAGCAAAGA TCTAAGGACG GTGACTGCAG

30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTATGTGTCT GAAAATGAGC GTGGAGATTG GGCTCGCAC

39

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCGAGCCC AATCTCCACG CTCATTTCA GACACATAC

39

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Tyr Gln Arg Thr Arg Ala Leu Val
 1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA	60
CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG	120
TTGGCGGGTG TCAGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC	180
ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGATTGG	240
CTATTGCCA TTGCATACGT TGTATCCATA TCATAATATG TACATTATA TTGGCTCATG	300
TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC	360
GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCCGTTC ACATAACTTA CGGTAAATGG	420
CCCGCCTGGC TGACCGCCCA ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC	480
CATAGTAACG CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC	540
TGCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA	600
TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTATGGG ACTTTCCCTAC	660
TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA	720
CATCAATGGG CGTGGATAGC GGTTGACTC ACGGGGATTT CCAAGTCTCC ACCCCATTGA	780
CGTCAATGGG AGTTTGTGTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA	840
CTCCGCCCA TTGACGCAA TGGCGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG	900
AGCTCGTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACCGCTGTT TTGACCTCCA	960

TAGAAGACAC CGGGACCGAT CCAGCCTCCG CGGCCGGAA CGGTGCATTG GAACGCGGAT	1020
TCCCCGTGCC AAGAGTGACG TAAGTACCGC CTATAGAGTC TATAGGCCA CCCCCCTTGGC	1080
TTCTTATGCA TGCTATACTG TTTTTGGCTT GGGGTCTATA CACCCCCGCT TCCTCATGTT	1140
ATAGGTGATG GTATAGCTTA GCCTATAGGT GTGGGTTATT GACCATTATT GACCACTCCC	1200
CTATTGGTGA CGATACTTTC CATTACTAAT CCATAACATG GCTCTTGCC ACAACTCTCT	1260
TTATTGGCTA TATGCCAATA CACTGTCCTT CAGAGACTGA CACGGACTCT GTATTTTAC	1320
AGGATGGGGT CTCATTTATT ATTTACAAAT TCACATATAC AACACCACCG TCCCCAGTGC	1380
CCGCAGTTT TATTAAACAT AACGTGGGAT CTCCACGCGA ATCTCGGGTA CGTGTTCGG	1440
ACATGGGCTC TTCTCCGGTA GCGGCGGAGC TTCTACATCC GAGCCCTGCT CCCATGCCTC	1500
CAGCGACTCA TGGTCGCTCG GCAGCTCCTT GCTCCTAACAA GTGGAGGCCA GACTTAGGCA	1560
CAGCACCGATG CCCACCACCA CCAGTGTGCC GCACAAGGCC GTGGCGGTAG GGTATGTGTC	1620
TGAAAATGAG CTCGGGGAGC GGGCTTGCAC CGCTGACGCA TTTGGAAGAC TTAAGGCAGC	1680
GGCAGAAGAA GATGCAGGCA GCTGAGTTGT TGTGTTCTGA TAAGAGTCAG AGGTAACCTCC	1740
CGTTGCGGTG CTGTTAACGG TGGAGGGCAG TGTAGTCTGA GCAGTACTCG TTGCTGCCGC	1800
GCGCGCCACC AGACATAATA GCTGACAGAC TAACAGACTG TTCCTTCCA TGGGTCTTTT	1860
CTGCAGTCAC CGTCCTTAGA TCTGCTGTGC CTTCTAGTTG CCAGCCATCT GTTGTTCGCC	1920
CCTCCCCGT GCCTTCCTTG ACCCTGGAAG GTGCCACTCC CACTGTCCTT TCCTAATAAA	1980
ATGAGGAAAT TGCATCGCAT TGTCTGAGTA GGTGTCATTC TATTCTGGGG GGTGGGGTGG	2040
GGCAGCACAG CAAGGGGGAG GATTGGGAAG ACAATAGCAG GCATGCTGGG GATGCGGTGG	2100
GCTCTATGGG TACCCAGGTG CTGAAGAATT GACCCGGTTC CTCCTGGGCC AGAAAGAAC	2160
AGGCACATCC CCTTCTCTGT GACACACCCT GTCCACGCCCT CTGGTTCTTA GTTCCAGGCC	2220
CACTCATAGG ACACTCATAG CTCAGGAGGG CTCCGCCTTC AATCCCACCC GCTAAAGTAC	2280
TTGGAGCGGT CTCTCCCTCC CTCATCAGCC CACCAAACCA AACCTAGCCT CCAAGAGTGG	2340
GAAGAAATTA AAGCAAGATA GGCTATTAAG TGCAGAGGGA GAGAAAATGC CTCCAACATG	2400
TGAGGAAGTA ATGAGAGAAA TCATAGAATT TCTTCCGCTT CCTCGCTCAC TGACTCGCTG	2460
CGCTCGGTG TTCGGCTGCG GCGAGCGGT A TCAGCTCACT CAAAGGCGGT AATACGGTTA	2520
TCCACAGAAT CAGGGATAA CGCAGGAAAG AACATGTGAG CAAAAGGCCA GCAAAGGCC	2580
AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCC CCCTGACGAG	2640
CATCACAAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAAC	2700

CAGGC GTTTC CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCCCT GCCGCTTACC	2760
GGATACCTGT CCGCCTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCAATG CTCACGCTGT	2820
AGGTATCTCA GTTCGGTGT A GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC	2880
GTTCAGCCCG ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA CCCGGTAAGA	2940
CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAAACAGGA TTAGCAGAGC GAGGTATGTA	3000
GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG AAGGACAGTA	3060
TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA	3120
TCCGGCAAAC AAACCACCGC TGGTAGCGGT GGTTTTTTG TTTGCAAGCA GCAGATTACG	3180
CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTTT CTACGGGTC TGACGCTCAG	3240
TGGAACGAAA ACTCACGTTA AGGGATTTG GTCATGAGAT TATCAAAAG GATCTTCACC	3300
TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA TGAGTAAACT	3360
TGGTCTGACA GTTACCAATG CTTAACAGT GAGGCACCTA TCTCAGCGAT CTGTCTATTT	3420
CGTTCATCCA TAGTTGCCTG ACTCCCCGTC GTCTAGATAA CTACGATACG GGAGGGCTTA	3480
CCATCTGGCC CCAGTGCTGC AATGATACCG CGAGACCCAC GCTCACCGGC TCCAGATTTA	3540
TCAGCAATAA ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC AACTTTATCC	3600
GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC GCCAGTTAAT	3660
AGTTTGCAGCA ACAGTTGTTGC CATTGCTACA GGCATCGTGG TGTCACGCTC GTCGTTGGT	3720
ATGGCTTCAT TCAGCTCCGG TTCCCAACGA TCAAGGCGAG TTACATGATC CCCCATGTTG	3780
TGCAAAAAAG CGGTTAGCTC CTTCGGTCTT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA	3840
GTGTTATCAC TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA	3900
AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA GTGTATGCGG	3960
CGACCGAGTT GCTCTTGCCTT GGCAGCAATA CGGGATAATA CCGCGCCACA TAGCAGAACT	4020
TTAAAAGTGC TCATCATTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG	4080
CTGTTGAGAT CCAGTTCGAT GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTTT	4140
ACTTTCACCA GCGTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAGGGA	4200
ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC TTTTCAATA TTATTGAAGC	4260
ATTATCAGG GTTATTGTCT CATGAGCGGA TACATATTG AATGTATTAA GAAAAATAAAA	4320
CAAATAGGGG TTCCGGCGAC ATTTCCCCGA AAAGTGCCAC CTGACGTCTA AGAAACCATT	4380

ATTATCATGA CATTAAACCTA TAAAAATAGG CGTATCACGA GGCCCTTCG TC 4432

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both.

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTGGCTATT GGCCATTGCA TACGTTGTAT CCATATCATA ATATGTACAT TTATATTGGC	60
TCATGTCCAA CATTACCGCC ATGTTGACAT TGATTATTGA CTAGTTATTA ATAGTAATCA	120
ATTACGGGGT CATTAGTTCA TAGCCCATAAT ATGGAGTTCC GCGTTACATA ACTTACGGTA	180
AATGGCCCGC CTGGCTGACC GCCAACGAC CCCCGCCCCAT TGACGTCAAT AATGACGTAT	240
GTTCCCATAG TAACGCCAAT AGGGACTTTC CATTGACGTC AATGGGTGGA GTATTTACGG	300
TAAACTGCCC ACTTGGCAGT ACATCAAGTG TATCATATGC CAAGTACGCC CCCTATTGAC	360
GTCAATGACG GTAAATGGCC CGCCTGGCAT TATGCCAGT ACATGACCTT ATGGGACTTT	420
CCTACTTGGC AGTACATCTA CGTATTAGTC ATCGCTATTA CCATGGTGAT GCGGTTTGG	480
CAGTACATCA ATGGGCGTGG ATAGCGTTT GACTCACGGG GATTCCAAG TCTCCACCCC	540
ATTGACGTCA ATGGGAGTTT GTTTGGCAC CAAAATCAAC GGGACTTCC AAAATGTCGT	600
AACAACCTCCG CCCCCATTGAC GCAAATGGC GGTAGGCGTG TACGGTGGGA GGTCTATATA	660
AGCAGAGCTC GTTTAGTGAA CCGTCAGATC GCCTGGAGAC GCCATCCACG CTGTTTGAC	720
CTCCATAGAA GACACCGGGA CCGATCCAGC CTCCGCGGCC GGGAACGGTG CATTGGAACG	780
CGGATTCCCC GTGCCAAGAG TGACGTAAGT ACCGCCTATA GAGTCTATAG GCCCACCCCC	840
TTGGCTTCTT ATGCATGCTA TACTGTTTT GGCTTGGGGT CTATACACCC CCGCTTCCTC	900
ATGTTATAGG TGATGGTATA GCTTAGCCTA TAGGTGTGGG TTATTGACCA TTATTGACCA	960
CTCCCCATT GGTGACGATA CTTTCCATTA CTAATCCATA ACATGGCTCT TTGCCACAAC	1020
TCTCTTTATT GGCTATATGC CAATACACTG TCCTTCAGAG ACTGACACGG ACTCTGTATT	1080

TTTACAGGAT GGGGTCTCAT TTATTATTTA CAAATTACA TATAAACAC CACCGTCCCC 1140
 AGTGCCCGCA GTTTTATTAA AACATAACGT GGGATCTCCA CGCGAATCTC GGGTACGTGT 1200
 TCCGGACATG GGCTCTTCTC CGGTAGCGGC GGAGCTTCTA CATCCGAGCC CTGCTCCCCT 1260
 GCCTCCAGCG ACTCATGGTC GCTCGGCAGC TCCTTGCTCC TAACAGTGGA GGCCAGACTT 1320
 AGGCACAGCA CGATGCCAC CACCACCAAGT GTGCCGCACA AGGCCGTGGC GGTAGGGTAT 1380
 GTGTCTGAAA ATGAGCTCGG GGAGCGGGCT TGACCCGCTG ACGCATTGG AAGACTTAAG 1440
 GCAGCGGCAG AAGAAGATGC AGGCAGCTGA GTTGTGTGT TCTGATAAGA GTCAGAGGTA 1500
 ACTCCCCTTG CGGTGCTGTT AACGGTGGAG GGCAAGTGTAG TCTGAGCAGT ACTCGTTGCT 1560
 GCCGCGCGCG CCACCAAGACA TAATAGCTGA CAGACTAACAA GACTGTTCT TTCCATGGGT 1620
 CTTTTCTGCA GTCACCGTCC TTAGATCTGC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT 1680
 TTGCCCTCC CCCGTGCCTT CCTTGACCCCT GGAAGGTGCC ACTCCCACGT TCCTTCCTA 1740
 ATAAAAATGAG GAAATTGCAT CGCATTGTCT GAGTAGGTGT CATTCTATTC TGGGGGGTGG 1800
 GGTGGGGCAG CACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC 1860
 GGTGGGCTCT ATGGGTACCC AGGTGCTGAA GAATTGACCC GGTTCCCTCCT GGGCCAGAAA 1920
 GAAGCAGGCA CATCCCCTTC TCTGTGACAC ACCCTGTCCA CGCCCTGGT TCTTAGTTCC 1980
 AGCCCCACTC ATAGGACACT CATAGCTCAG GAGGGCTCCG CCTTCAATCC CACCCGCTAA 2040
 AGTACTTGGA GCGGTCTCTC CCTCCCTCAT CAGCCCACCA AACCAAACCT AGCCTCCAAG 2100
 AGTGGGAAGA ATTAAAGCA AGATAGGCTA TTAAGTGCAG AGGGAGAGAA AATGCCTCCA 2160
 ACATGTGAGG AAGTAATGAG AGAAATCATA GAATTC 2196

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTAGA TAATCACTCA CTGAGTGACA 60
 TCAAAATCAT G 71

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACCGTCCTTA GATCAGCTTG GCAAAAGCAG GCAAACCATT TGAATGGATG TCAATCCGAC 60
 CTTACTTTTC TTAAAAGTGC CAGCACAAAA TGCTATAAGC ACAACTTTCC CTTATAC 117

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTGAC AAAAACATAA TGGATCCAAA 60
 CACTGTGTCA AGCTTCAGG TAGATTGCTT TCTTTGGCAT GTCCGCAAAC GAGTTGCAGA 120
 CCAAGAACTA GGTGAT 136

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCTGCAGTCA CCGTCCTTAG ATCAGCTTGG AGCAAAAGCA GGGGAAAATA AAAACAACCA	60
AAATGAAGGC AAACCTACTG GTCCTGTTAA GTGCACTTGC AGCTGCAGAT GCAGACACAA	120
TATGTATAGG CTACCATGCG AACAAATTCAA CC	152

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTTCTGCAG TCACCGTCCT TAGATCCCGA ATTCCAGCAA AAGCAGGTCA ATTATATTCA	60
ATATGGAAAG AATAAAAGAA CTAAGAAATC TAATGTCGCA GTCTGCCACC CCGGAGATAC	120
TCACAAAAAC CACCGTGGAC CATATGGCCA TAATCAAGAA GT	162

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCACCGTCC TTAGATCTAC CATGAGTCTT CTAACCGAGG TCGAAACGTA CGTACTCTCT	60
ATCATCCCGT CAGGCCCCCT CAAAGCCGAG ATCGCACAGA GACTTGAAAGA GTTGACGGAA	120
GA	122

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA	60
CAGCTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG TCAGGGCGCG TCAGCGGGTG	120
TTGGCGGGTG TCGGGGCTGG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC	180
ACCATATGCG GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGATTGG	240
CTATTGGCCA TTGCATACGT TGTATCCATA TCATAATATG TACATTTATA TTGGCTCATG	300
TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC	360
GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCCGCGTT ACATAACTTA CGGTAAATGG	420
CCCGCCTGGC TGACCGCCCA ACGACCCCCG CCCATTGACCG TCAATAATGA CGTATGTTCC	480
CATAGTAACG CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGAGTATT TACGGTAAAC	540
TGCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA TTGACGTCAA	600
TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTATGGG ACTTTCCTAC	660
TTGGCAGTAC ATCTACGTAT TAGTCATCGC TATTACCATG GTGATGCGGT TTTGGCAGTA	720
CATCAATGGG CGTGGATAGC GGTTTGAECTC ACGGGGATTTC CCAAGTCTCC ACCCCATTGA	780
CGTCAATGGG AGTTTGTGTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA	840
CTCCGCCCA TTGACGCAA TGGCGGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG	900

AGCTCGTTA	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCA	CCCCCTTGGC	1080
TTCTTATGCA	TGCTATACTG	TTTTGGCTT	GGGGTCTATA	CACCCCCGCT	TCCTCATGTT	1140
ATAGGTGATG	GTATAGCTTA	GCCTATAGGT	GTGGGTTATT	GACCATTATT	GACCACTCCC	1200
CTATTGGTGA	CGATACTTTC	CATTACTAAT	CCATAAACATG	GCTCTTGCC	ACAACCTCT	1260
TTATTGGCTA	TATGCCAATA	CACTGTCCTT	CAGAGACTGA	CACGGACTCT	GTATTTTAC	1320
AGGATGGGGT	CTCATTATTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
CCGCAGTTTT	TATTAAACAT	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCGG	1440
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC	TTCTACATCC	GAGCCCTGCT	CCCATGCCTC	1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACCA	GTGGAGGCCA	GAATTAGGCA	1560
CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620
TGAAAATGAG	CTCGGGGAGC	GGGCTTGCAC	CGCTGACGCA	TTTGGAAAGAC	TTAAGGCAGC	1680
GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACCTCC	1740
CGTTGCGGTG	CTGTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
GCGCGCCACC	AGACATAATA	GCTGACAGAC	TAACAGACTG	TTCCCTTCCA	TGGGTCTTTT	1860
CTGCAGTCAC	CGTCCTTAGA	TCTGCTGTGC	CTTCTAGTTG	CCAGCCATCT	GTGTTTGCC	1920
CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GTGCCACTCC	CACTGTCCTT	TCCTAACAAA	1980
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCAATT	TATTCTGGGG	GGTGGGGTGG	2040
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	2100
GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	AGAAAGAAGC	2160
AGGCACATCC	CCTTCTCTGT	GACACACCCT	GTCCACGCC	CTGGTTCTTA	GTTCAGCCC	2220
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTG	TTCGGCTGCG	GCGAGCGGT	TCAGCTCACT	CAAAGGCCGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580

AGGAACCGTA AAAAGGCCGC GTTGCTGGCG TTTTCCATA GGCTCCGCC CCCTGACGAG	2640
CATCACAAAA ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAC	2700
CAGGCCTTTC CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCCCT GCCGCTTACC	2760
GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC TTTCTCAATG CTCACGCTGT	2820
AGGTATCTCA GTTCGGTGTA GGTCGTTCGC TCCAAGCTGG GCTGTGTGCA CGAACCCCCC	2880
GTTCAGCCCC ACCGCTGCGC CTTATCCGGT AACTATCGTC TTGAGTCCAA CCCGGTAAGA	2940
CACGACTTAT CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC GAGGTATGTA	3000
GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG AAGGACAGTA	3060
TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG TAGCTCTTGA	3120
TCCGGCAAAC AAACCACCGC TGGTAGCGGT GGTTTTTTTG TTTGCAAGCA GCAGATTACG	3180
CGCAGAAAAA AAGGATCTCA AGAAGATCCT TTGATCTTT CTACGGGTC TGACGCTCAG	3240
TGGAACGAAA ACTCACGTTA AGGGATTTG GTCATGAGAT TATCAAAAAG GATCTTCACC	3300
TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA TGAGTAAACT	3360
TGGTCTGACA GTTACCAATG CTTAACAGT GAGGCACCTA TCTCAGCGAT CTGTCTATT	3420
CGTTCATCCA TAGTTGCCTG ACTCCGGGG GGGGGGGCGC TGAGGTCTGC CTCGTGAAGA	3480
AGGTGTTGCT GACTCATACC AGGCCTGAAT CGCCCCATCA TCCAGCCAGA AAGTGAGGGA	3540
GCCACGGTTG ATGAGAGCTT TGTTGTAGGT GGACCAGTTG GTGATTTGA ACTTTTGCTT	3600
TGCCACGGAA CGGTCTGCGT TGTCGGGAAG ATGCGTGATC TGATCCTTCA ACTCAGCAAA	3660
AGTTCGATTT ATTCAACAAA GCCGCCGTCC CGTCAAGTCA GCGTAATGCT CTGCCAGTGT	3720
TACAACCAAT TAACCAATTG TGATTAGAAA AACTCATCGA GCATCAAATG AACTGCAAT	3780
TTATTCATAT CAGGATTATC AATACCATAT TTTTGAAAAA GCCGTTCTG TAATGAAGGA	3840
GAAAACTCAC CGAGGCAGTT CCATAGGATG GCAAGATCCT GGTATCGGTC TGCGATTCCG	3900
ACTCGTCCAA CATCAATACA ACCTATTAAT TTCCCTCGT CAAAAATAAG GTTATCAAGT	3960
GAGAAATCAC CATGAGTGAC GACTGAATCC GGTGAGAATG GCAAAAGCTT ATGCATTTCT	4020
TTCCAGACTT GTTCAACAGG CCAGCCATTA CGCTCGTCAT CAAAATCACT CGCATCAACC	4080
AAACCGTTAT TCATTCGTGA TTGCGCCTGA GCGAGACGAA ATACCGGATC GCTGTTAAAA	4140
GGACAATTAC AAACAGGAAT CGAATGCAAC CGGCGCAGGA ACACTGCCAG CGCATCAACA	4200
ATATTTTCAC CTGAATCAGG ATATTCTTCT AATACCTGGA ATGCTGTTTT CCCGGGGATC	4260

GCAGTGGTGA	GTAACCATGC	ATCATCAGGA	GTACGGATAA	AATGCTTGAT	GGTCGGAAGA	4320
GGCATAAATT	CCGTCAGCCA	GTTTAGTCTG	ACCATCTCAT	CTGTAACATC	ATTGGCAACG	4380
CTACCTTGC	CATGTTTCAG	AAACAACCTCT	GGCGCATCGG	GCTTCCCATA	CAATCGATAG	4440
ATTGTCGCAC	CTGATTGCC	GACATTATCG	CGAGCCCATT	TATAACCCATA	TAAATCAGCA	4500
TCCATGTTGG	AATTTAACATCG	CGGCCTCGAG	CAAGACGTTT	CCC GTTGAAT	ATGGCTCATA	4560.
ACACCCCTTG	TATTACTGTT	TATGTAAGCA	GACAGTTTTA	TTGTTCATGA	TGATATATTT	4620
TTATCTTGTG	CAATGTAACA	TCAGAGATTT	TGAGACACAA	CGTGGCTTTC	CCCCCCCCCC	4680
CATTATTGAA	GCATTTATCA	GGGTTATTGT	CTCATGAGCG	GATACATATT	TGAATGTATT	4740
TAGAAAAATA	AACAAATAGG	GGTTCCGCGC	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC	4800
TAAGAAACCA	TTATTATCAT	GACATTAACC	TATAAAAATA	GGCGTATCAC	GAGGCCCTTT	4860
CGTC						4864

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAGAAAGCA GAGCA

15

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCACCGTCCT TAGATCAAGC AGGGTTAATA ATCACTCACT GAGTGACATC AAAATCATGG	60
CGTCCCAAGG CACCAAACGG TCTTATGAAC AGATGGAAAC TGATGGGAA CGCCAGATT	119

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGGGGCAAA CAACAGATGG CTGGCAACTA GAAGGCACAG CAGATATTTC TTCCCTTAATT	60
GTCGTAC	67

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCAGAAGCA CGCAC 15

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCAGAAAGCA CAGCA

15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCTTAGATCG GAAATAAAAA CAACCAAAAT GAA

33

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAGATCCTT ATATTCTGA AATTCTGGTC TCAGAT

36

(2) INFORMATION FOR SEQ ID NO:26:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACCGTCCTTA GATCCAGAAG CAGAGCATT TCTAATATCC ACAAAATGAA GGCAATAATT 60

GTACTACTCA TGGTAGTAAC ATCCAACGCA GATCGAATCT GC 102

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGCACAGCAG ATCTTTCAAT AACGTTCTT TGTAATGGTA AC 42

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAACAGACT GTTCCTTCC ATG

23

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGAGTGGCAC CTTCCAGG

18

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCAAAAGCA GG

12

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGCAGAAGCG GAGC

14

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCACATGTCG ACCCGTAAAA AGGCCGGT GCTGG

35

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACAACCA TGAAGACTAT CATTGCTTTG AGC

33

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCACATAGAT CTTCAAATGC AAATGTTGCA CCTAATG

37

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTACAACCA TGAAAGCAAA ACTACTAGTC CTGTTATG

38

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCACATTCAAG ATGCATATTC TACACTGCAA AG

32

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTACAACCA TGAAGGCAAT AATTGTACTA CTCATG

36

(2) INFORMATION FOR SEQ ID NO:38:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCACATTTAT AGACAGATGG AGCAAGAAC ATTGTC

36

(2) INFORMATION FOR SEQ ID NO:39:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGTACAAGAT CTACCATGCT TCTAACCGAG GTC

33

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC

36

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGTACAGGAT CCACCATGTC CAACATGGAT ATTGACGGC

39

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCACATGGAT CCTTAATAAT CGAGGTCATC ATAATCCTC

39

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTACAGGAT CCACCATGTC GCTGTTGGA GACACAATTG CC

42

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCACATGGAT CCTTATAGGT ATTTCTTCAC AAGAGCTG

38

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3553 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATATTGGCT ATTGGCCATT GCATACGTTG TATCCATATC ATAATATGTA CATTATATT	60
GGCTCATGTC CAACATTACC GCCATGTTGA CATTGATTAT TGACTAGTTA TTAATAGTAA	120
TCAATTACGG GGTCATTAGT TCATAGCCC A TATGGAGT TCCGCCTAC ATAAC TTACG	180
GTAAATGGCC CGCCTGGCTG ACCGCCAAC GACCCCCGCC CATTGACGTC AATAATGACG	240
TATGTTCCA TAGTAACGCC AATAGGGACT TTCCATTGAC GTCAATGGGT GGAGTATTAA	300
CGGTAAACTG CCCACTTGCG AGTACATCAA GTGTATCATA TGCCAAGTAC GCCCCCTATT	360
GACGTCAATG ACGTAAATG GCGCGCTGG CATTATGCC AGTACATGAC CTTATGGGAC	420
TTTCCTACTT GGCAGTACAT CTACGTATTA GTCATCGCTA TTACCATGGT GATGCGTTT	480
TGGCAGTACA TCAATGGCG TGGATAGCGG TTTGACTCAC GGGGATTCC AAGTCTCCAC	540
CCCATTGACG TCAATGGGAG TTTGTTTGG CACCAAAATC AACGGGACTT TCCAAAATGT	600
CGTAACAACT CGCCCCATT GACGCAAATG GCGGTAGGC GTGTACGGT GGAGGTCTAT	660
ATAAGCAGAG CTCGTTAGT GAACCGTCAG ATCGCCTGGA GACGCCATCC ACGCTGTTT	720
GACCTCCATA GAAGACACCG GGACCGATCC AGCCTCCGCG GCCGGGAACG GTGCATTGGA	780
ACGCGGATTC CCCGTGCCAA GAGTGACGTA AGTACCGCCT ATAGAGTCTA TAGGCCACC	840
CCCTTGGCTT CTTATGCATG CTATACTGTT TTTGGCTTGG GGTCTATACA CCCCCGCTTC	900
CTCATGTTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTTATTGA CCATTATTGA	960
CCACTCCCC ATTGGTGACG ATACTTCCA TTACTAATCC ATAACATGGC TCTTGCCAC	1020
AACTCTCTT ATTGGCTATA TGCCAATACA CTGTCCTTCA GAGACTGACA CGGACTCTGT	1080
ATTTTTACAG GATGGGGTCT CATTATTAT TTACAAATTC ACATATACAA CACCACCGTC	1140
CCCAGTGCC C GAGTTTTA TTAAACATGC TAACGTGGGA TCTCCACGCG AATCTCGGGT	1200
ACGTGTTCCG GACATGGCT CTTCTCCGGT AGCGGCGGAG CTTCTACATC CGAGCCCTGC	1260
TCCCAGTGCCT CCAGCGACTC ATGGTCGCTC GGCAGCTCCT TGCTCCTAAC AGTGGAGGCC	1320
AGACTTAGGC ACAGCACGAT GCCCACCACC ACCAGTGTGC CGCACAAAGC CGTGGCGGTA	1380
GGGTATGTGT CTGAAAATGA GCTCGGGAG CGGGCTTGCA CCGCTGACGC ATTTGGAAGA	1440
CTTAAGGCAG CGGCAGAAGA AGATGCAGGC AGCTGAGTTG TTGTGTTCTG ATAAGAGTCA	1500
GAGGTAACTC CCGTTGCGGT GCTGTTAACG GTGGAGGGCA GTGTAGTCTG AGCAGTACTC	1560
GTTGCTGCCG CGCGCGCCAC CAGACATAAT AGCTGACAGA CTAACAGACT GTTCCTTTCC	1620

ATGGGTCTTT	TCTGCAGTCA	CCGTCCTTAG	ATCTGCTGTG	CCTTCTAGTT	GCCAGCCATC	1680
TGTTGTTGC	CCCTCCCCCG	TGCCTTCCTT	GACCCCTGGAA	GGTGCCACTC	CCACTGTCCT	1740
TTCCTAATAA	AATGAGGAAA	TTGCATCGCA	TTGTCTGAGT	AGGTGTCATT	CTATTCTGGG	1800
GGGTGGGTG	GGGCAGCACA	GCAAGGGGGA	GGATTPGGAA	GACAATAGCA	GGCATGCTGG	1860
GGATGCGGTG	GGCTCTATGG	GTACGGCCGC	AGCGGCCGTA	CCCAGGTGCT	GAAGAATTGA	1920
CCCGGTTCC	CGACCCGTAA	AAAGGCCGCG	TTGCTGGCGT	TTTTCATAG	GCTCCGCC	1980
CCTGACGAGC	ATCACAAAAAA	TCGACGCTCA	AGTCAGAGGT	GGCGAAACCC	GACAGGACTA	2040
TAAAGATACC	AGGC GTTCC	CCCTGGAAGC	TCCCTCGTGC	GCTCTCCTGT	TCCGACCCCTG	2100
CCGCTTACCG	GATA CCTGTC	CGCCTTCTC	CCTTCGGAA	GC GTGGCGCT	TTCTCAATGC	2160
TCACGCTGTA	GGTATCTCAG	TTCGGTGTAG	GTCGTTCGCT	CCAAGCTGGG	CTGTGTGCAC	2220
GAACCCCCCG	TTCAGCCCGA	CCGCTGCGCC	TTATCCGTA	ACTATCGTCT	TGAGTCCAAC	2280
CCGGTAAGAC	ACGACTTATC	GCCACTGGCA	GCAGCCACTG	GTAACAGGAT	TAGCAGAGCG	2340
AGGTATGTAG	GCGGTGCTAC	AGAGTTCTTG	AA GTGGTGGC	CTAACTACGG	CTACACTAGC	2400
TGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT	2460
GGTAGCTCTT	GATCCGGCAA	ACAAACCACC	GCTGGTAGCG	GTGGTTTTTT	TGTTGCAAG	2520
CAGCAGATTA	CGCGCAGAAA	AAAAGGATCT	CAAGAAGATC	CTTGATCTT	TTCTACGTGA	2580
TCCC GTAATG	CTCTGCCAGT	GTTACAACCA	ATTAACCAAT	TCTGATTAGA	AAA ACTCATC	2640
GAGCATCAA	TGAAACTGCA	ATTTATT CAT	ATCAGGATTA	TCAATACCAT	ATTTTGAAA	2700
AAGCCGTTTC	TGTAATGAAG	GAGAAA ACTC	ACCGAGGCAG	TTCCATAGGA	TGGCAAGATC	2760
CTGGTATCGG	TCTGCGATTC	CGACTCGTCC	AACATCAATA	CAACCTATTA	ATT TCCCCTC	2820
GTCAAAAATA	AGGTTATCAA	GTGAGAAATC	ACCATGAGTG	ACGACTGAAT	CCGGTGAGAA	2880
TGGCAAAAGC	TTATGCATTT	CTTTCCAGAC	TTGTTCAACA	GGCCAGCCAT	TACGCTCGTC	2940
ATCAAAATCA	CTCGCATCAA	CCAAACCGTT	ATTCATT CGT	GATTGCGCCT	GAGCGAGACG	3000
AAATACGCGA	TCGCTGTTAA	AAGGACAATT	ACAAACAGGA	ATCGAATGCA	ACCGGCGCAG	3060
GAACACTGCC	AGCGCATCAA	CAATATTTTC	ACCTGAATCA	GGATATTCTT	CTAATACCTG	3120
GAATGCTGTT	TTCCCGGGGA	TCGCAGTGGT	GAGTAACCAT	GCATCATCAG	GAGTACGGAT	3180
AAAATGCTTG	ATGGTCGGAA	GAGGCATAAA	TTCCGT CAGC	CAGTTAGTC	TGACCATCTC	3240
ATCTGTAACA	TCATTGGCAA	CGCTACCTTT	GCCATGTTTC	AGAAACAAC	CTGGCGC ATC	3300

GGGCTTCCA TACAATCGAT AGATTGTCGC ACCTGATTGC CCGACATTAT CGCGAGCCCA	3360
TTTATAACCA TATAAATCAG CATCCATGTT GGAATTAAAT CGCGGCCTCG AGCAAGACGT	3420
TTCCCCTTGA ATATGGCTCA TAACACCCCT TGTATTACTG TTTATGTAAG CAGACAGTTT	3480
TATTGTTCAT GATGATATAT TTTTATCTTG TGCAATGTAA CATCAGAGAT TTTGAGACAC	3540
AACGTGGCTT TCC	3553

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCACCGTCCT TAGATCGGTA CAACCATGAA GACTATCATT GCTTGAGCT ACATTTATG	60
TCTGGTTTTC GC	72

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCATGCTTT TGCTTTGTGT TGTTTGCTG GGGTTCATCA TGTGGGCCTG CCAAAAAGGC	60
AACATTAGGT GCAACATTTG CATTGAAGA TCTATGTGGG ATCTGCTGTG C	111

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TTAGATCGGA ACATGAAAGC AAAACTACTA GTCCTGTTAT GTGCATTAC AGCTACATAT	60
GCA	63

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGGTGCTTT TGGTCTCCCT GGGGGCAATC AGCTTCTGGA TGTGTTCTAA TGGGTCTTG	60
CAGTGTAGAA TATGCATCTG AATGTGGGAT CTGCTGTGCC TT	102

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCTTAGATCG GTACAACCAT GAAGGCAATA ATTGTACTAC TCATGGTAGT AACATCCAAC	60
GCAGATCGAA TCTGCACTGG GATAACATCT TCAAACTCAC CTCATGTG	108

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTGGCTGTA CATTGATGAT AGCTATTTT ATTGTTTATA TGGTCTCCAG AGACAATGTT	60
TCTTGCTCCA TCTGTCTATA AATGTGGGAT CTGCTGTGCC TT	102

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTCCTTAGAT CCACCATGGC GTCCAAGGC ACCAACGGT CTTATGAACA GATGGAAACT	60
GATGGGAAAC GCCAGAATGC AACT	84

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAAAAGGCAA CGAACCCGAT CGTGCCTCT TTTGACATGA GTAATGAAGG ATCTTATTTC	60
TTCGGAGACA ATGCAGAAGA GTACGACAAT TAAGGATCTG CTGTGCCT	108

(2) INFORMATION FOR SEQ ID NO:54

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTTAGATCCA GATCTACCCT GAGTCTTCTA ACCGAGGTCG AAACGTATGT TCTCTCTATC	60
GTTCCATCAG GCCCCCTCAA AGCCGAAATC GCGCAGAGAC TTGAAGATGT CTTTGCTGGG	120
AAAAACACAG AT	132

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
 GGGACTCATC CTAGCTCCAG TACTGGTCTA AAAGATGATC TTCTTGAAAA TTTGCAGACC 60
 TATCAGAAC GAATGGGGGT GCAGATGCAA CGGTTCAAGT GAAGATCTAT GTGGGATCTG 120
 CTGTGCCTT 129

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTTAGATCCA CCATGTCCAA CATGGATATT GACGGTATCA ACACTGGGAC AATTGACAAA 60
 ACACCGGAAG AAATAACTTC T 81

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTTGAAATTCA CAATTAAGCA GACCATCCCC AATTTCTTCT TTGGGAGGGCA CACAGCAGAG 60
 GATTATGATG ACCTCGATTAA TTAAGGATCT GCTGTG 96

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTTAGATCCA CCATGTCGCT GTTTGGAGAC ACAATTGCCT ACCTGCTTTC ATTGACAGAA	60
---	----

GATGGAGAAG GCAAAGCAGA ACTAGCAGAA AAATTA	96
---	----

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGATCTCTTG GGGCAAGTCA AGAGAAATGGG GAAGGAATTG CAAAGGATGT GATGGAAGTG	60
--	----

CTAAAGCAGA GCTCTATGGG AAATTCAGCT CTTGTGAAGA AATAACCTATA AGGATCTGCT	120
--	-----

GTG	123
-----	-----

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGTACAAATA TTGCTATTG GCCATTGCAT ACG

33

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCACATCTCG AGGAACCGGG TCAATTCTTC AGCACCC

36

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGTACAGATA TCGGAAAGCC ACGTTGTGTC TCAAAATC

38

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCACATGGAT CCGTAATGCT CTGCCAGTGT TACAACC

37

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGTACATGAT CACGTAGAAA AGATCAAAGG ATCTTCTTG

39